

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 ggctcgggcg gtggtgggtc ggggtggcggc ggatcgtcac aggtgcagct gaagcagtc 480  
 ggacctggcc tagtgcagtc ctacacagagc ctgtccatca cctgcacagt ctctggtttc 540  
 tcattaacta cctatgctgt acactgggtt cgccagcttc caggaaagg tctggagtgg 600  
 ctgggagtga tatggagtgg tggaaacaca gactataatg cagctttcat atccagactg 660  
 agcatcacca aggacgattc caagagccaa gttttcttta aaatgaacag tctgcaacct 720  
 aatgacacag ccatttatta ctgtgccaga aatgggggtg ataactaccc ttattactat 780  
 gctatggact actgggggtca aggaacctca gtcaccgtct cctct 825

<210> 357  
 <211> 1536  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 357  
 aagcttgccg ccatgaggtt ctctgctcag cttctggggc tgcttgtgct ctggatccct 60  
 ggatccactg cagatattgt gatgacgcag gctgcattct ccaatccagt cactcttgga 120  
 acatcagctt ccattctctg cagggtctagt aagagtctcc tacatagtaa tggcatcact 180  
 tatttgtatt ggtatctgca gaagccaggc cagtctcttc agctcctgat ttatcagatg 240  
 tccaaccttg cctcaggagt ccagacagg tttagtagca gtgggtcagg aactgatttc 300  
 acactgagaa tcagcagagt ggaggctgag gatgtgggtg ttattactg tgctcaaaat 360  
 ctagaacttc cgctcacgtt cgggtgctggg accaagctgg agctgaaacg ggggtggcgg 420  
 ggctcgggcg gtggtgggtc ggggtggcggc ggatcgtcac aggtgcagct gaagcagtc 480  
 ggacctggcc tagtgcagtc ctacacagagc ctgtccatca cctgcacagt ctctggtttc 540  
 tcattaacta cctatgctgt acactgggtt cgccagcttc caggaaagg tctggagtgg 600  
 ctgggagtga tatggagtgg tggaaacaca gactataatg cagctttcat atccagactg 660  
 agcatcacca aggacgattc caagagccaa gttttcttta aaatgaacag tctgcaacct 720  
 aatgacacag ccatttatta ctgtgccaga aatgggggtg ataactaccc ttattactat 780  
 gctatggact actgggggtca aggaacctca gtcaccgtct cctctgatca ggagccaaa 840  
 tcttctgaca aaactcacac atccccaccg tccccagcac ctgaactcct ggggggaccg 900  
 tcagtcttcc tcttcccccc aaaacccaag gacacctca tgatctccc gacccttag 960  
 gtcacatgcg tgggtgggtg cgtgagccac gaagacctg aggtcaagtt caactgggtac 1020  
 gtggacggcg tggaggtgca taatgccaa gacaaagccg ctgacccagg gggaggagca gtacaacagc 1080  
 acgtaccgtg tggtcagcgt cctcaccgtc ctgacccagg actggctgaa tggcaaggag 1140  
 tacaagtgca aggtctccaa caaagccctc ccagcccca tcgagaaaac aatctccaaa 1200  
 gccaaaggcg agccccgaga accacaggtg tacacctgct ccccatccc ggatgagctg 1260  
 accaagaacc aggtcagcct gacctgctg gtcaaaggct tctatcccag cgacatcgcc 1320  
 gtggagtggg agagcaatgg gcagccggag aacaactaca agaccagcc tcccgtgctg 1380  
 gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440  
 caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgag 1500  
 aagagcctct ccctgtctcc gggtaaatga tctaga 1536

<210> 358  
 <211> 1696  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 358  
 aagcttgccg ccatgaggtt ctctgctcag cttctggggc tgcttgtgct ctggatccct 60  
 ggatccactg cagatattgt gatgacgcag gctgcattct ccaatccagt cactcttgga 120  
 acatcagctt ccattctctg cagggtctagt aagagtctcc tacatagtaa tggcatcact 180  
 tatttgtatt ggtatctgca gaagccaggc cagtctcttc agctcctgat ttatcagatg 240  
 tccaaccttg cctcaggagt ccagacagg tttagtagca gtgggtcagg aactgatttc 300  
 acactgagaa tcagcagagt ggaggctgag gatgtgggtg ttattactg tgctcaaaat 360  
 ctagaacttc cgctcacgtt cgggtgctggg accaagctgg agctgaaacg ggggtggcgg 420  
 ggctcgggcg gtggtgggtc ggggtggcggc ggatcgtcac aggtgcagct gaagcagtc 480  
 ggacctggcc tagtgcagtc ctacacagagc ctgtccatca cctgcacagt ctctggtttc 540  
 tcattaacta cctatgctgt acactgggtt cgccagcttc caggaaagg tctggagtgg 600  
 ctgggagtga tatggagtgg tggaaacaca gactataatg cagctttcat atccagactg 660  
 agcatcacca aggacgattc caagagccaa gttttcttta aaatgaacag tctgcaacct 720  
 aatgacacag ccatttatta ctgtgccaga aatgggggtg ataactaccc ttattactat 780  
 gctatggact actgggggtca aggaacctca gtcaccgtct cctctgatca ggagccaaa 840  
 tcttctgaca aaactcacac aagccaccg agccagcac ctgaactcct ggggggacg 900  
 tcagtcttcc tcttcccccc aaaacccaag gacacctca tgatctccc gacccttag 960

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactgggtac 1020  
 gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1080  
 acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1140  
 tacaagtgca aggtctccaa caaagccctc ccagcccca tcgagaaaac catctccaaa 1200  
 gccaaaggcg agcccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1260  
 accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1320  
 gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1380  
 gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440  
 caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1500  
 aagagcctct ccctgtctcc gggtaaagcg gatccttcga acctgctccc atcctgggcc 1560  
 attaccttaa tctcagtaaa tggaattttt gtgatatgct gcctgaccta ctgctttgcc 1620  
 ccaagatgca gagagagaag gaggaatgag agattgagaa gggaaagtgt acgcctctga 1680  
 taaatcgata ctcgag 1696

<210> 359  
 <211> 141  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 359  
 Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys  
 1 5 10 15  
 Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln  
 20 25 30  
 Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu  
 35 40 45  
 Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala  
 65 70 75 80  
 Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys Ser Gln  
 85 90 95  
 Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr  
 100 105 110  
 Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Ala Met  
 115 120 125  
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
 130 135 140

<210> 360  
 <211> 122  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 360  
 Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Ser Ser Gln  
 1 5 10 15  
 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr  
 20 25 30  
 Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu  
 35 40 45  
 Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala Ala Phe Ile  
 50 55 60  
 Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys Ser Gln Val Phe Phe  
 65 70 75 80  
 Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr Tyr Cys Ala  
 85 90 95  
 Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr Ala Met Asp Tyr Trp  
 100 105 110  
 Gly Gln Gly Thr Ser Val Thr Val Ser Ser

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
115 120

<210> 361  
<211> 133  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 361  
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro  
1 5 10 15  
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro  
20 25 30  
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Lys Ser  
35 40 45  
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys  
50 55 60  
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala  
65 70 75 80  
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe  
85 90 95  
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
100 105 110  
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys  
115 120 125  
Leu Glu Leu Lys Arg  
130

<210> 362  
<211> 271  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 362  
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro  
1 5 10 15  
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro  
20 25 30  
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Lys Ser  
35 40 45  
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys  
50 55 60  
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala  
65 70 75 80  
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe  
85 90 95  
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
100 105 110  
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys  
115 120 125  
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly  
130 135 140  
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu  
145 150 155 160  
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe  
165 170 175  
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys  
180 185 190  
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr  
195 200 205

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys  
 210 215 220  
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala  
 225 230 235 240  
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr  
 245 250 255  
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
 260 265 270

<210> 363  
 <211> 505  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 363  
 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro  
 1 5 10 15  
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro  
 20 25 30  
 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser  
 35 40 45  
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys  
 50 55 60  
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala  
 65 70 75 80  
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe  
 85 90 95  
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
 100 105 110  
 Cys Ala Gln Asn Leu Glu Leu Pro Thr Phe Gly Ala Gly Thr Lys  
 115 120 125  
 Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly  
 130 135 140  
 Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu  
 145 150 155 160  
 Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe  
 165 170 175  
 Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys  
 180 185 190  
 Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr  
 195 200 205  
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys  
 210 215 220  
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala  
 225 230 235 240  
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr  
 245 250 255  
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp  
 260 265 270  
 Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Ser Pro  
 275 280 285  
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 290 295 300  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 305 310 315 320  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
 325 330 335  
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 340 345 350  
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
 355 360 365  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 370 375 380  
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 385 390 395 400  
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
 405 410 415  
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
 420 425 430  
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
 435 440 445  
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 450 455 460  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 465 470 475 480  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 485 490 495  
 Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 500 505

<210> 364  
 <211> 556  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 364  
 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro  
 1 5 10 15  
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro  
 20 25 30  
 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser  
 35 40 45  
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys  
 50 55 60  
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala  
 65 70 75 80  
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe  
 85 90 95  
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
 100 105 110  
 Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys  
 115 120 125  
 Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly  
 130 135 140  
 Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu  
 145 150 155 160  
 Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe  
 165 170 175  
 Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys  
 180 185 190  
 Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr  
 195 200 205  
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys  
 210 215 220  
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala  
 225 230 235 240  
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr  
 245 250 255  
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp  
 260 265 270  
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Ser Pro  
 275 280 285  
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys  
 290 295 300  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 305 310 315 320  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
 325 330 335

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
340 345 350  
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
355 360 365  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
370 375 380  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
385 390 395 400  
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
405 410 415  
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
420 425 430  
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
435 440 445  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
450 455 460  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
465 470 475 480  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
485 490 495  
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu  
500 505 510  
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile  
515 520 525  
Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg  
530 535 540  
Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val  
545 550 555

<210> 365  
<211> 72  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo to introduce mutation in CH3 at position  
405 XX to Y

<400> 365  
gttggtgaag acgttcccct gctgccacct gctcttgctc acggtgagct tgctgtagag 60  
gtagaaggag cc 72

<210> 366  
<211> 72  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo to introduce mutation in CH3 at position  
405 XX to A

<400> 366  
gttggtgaag acgttcccct gctgccacct gctcttgctc acggtgagct tgctgtagag 60  
ggcgaaggag cc 72

<210> 367  
<211> 72  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo to introduce mutation in CH3 at position  
407 XX to A

<400> 367

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
gttggtgaag acgttcccct gctgccacct gctcttgcc acggtgagct tgctggcgag 60  
gaagaaggag cc 72

<210> 368  
<211> 72  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo to introduce mutation in CH3 at position  
405 XX to Y and 407 to A

<400> 368  
gttggtgaag acgttcccct gctgccacct gctcttgcc acggtgagct tgctggcgag 60  
gtagaaggag cc 72

<210> 369  
<211> 72  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo to introduce mutation in CH3 at position  
405 XX to A and 407 to Y

<400> 369  
gttggtgaag acgttcccct gctgccacct gctcttgcc acggtgagct tgctggcgag 60  
ggcgaaggag cc 72

<210> 370  
<211> 324  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 370  
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 60  
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 120  
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 180  
gacggctcct tctacctcta tagcaagctc accgtggaca agagcagggtg gcagcagggg 240  
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300  
ctctccctgt ccccggttaa atga 324

<210> 371  
<211> 324  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 371  
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 60  
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 120  
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 180  
gacggctcct tcgacctcta tagcaagctc accgtggaca agagcagggtg gcagcagggg 240  
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300  
ctctccctgt ccccggttaa atga 324

<210> 372  
<211> 324  
<212> DNA  
<213> Artificial Sequence

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polynucleotide

<400> 372

gggcagcccc	gagaaccaca	ggtgtacacc	ctgcccccat	cccgggagga	gatgaccaag	60
aaccagggtca	gcctgacctg	cctgggtcaaa	ggcttctatc	ccagcgacat	cgccgtggag	120
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgctccccgt	gctggactcc	180
gacggctcct	tcttcctcgc	cagcaagctc	accgtggaca	agagcagggtg	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
ctctccctgt	ccccgggtaa	atga				324

<210> 373

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 373

gggcagcccc	gagaaccaca	ggtgtacacc	ctgcccccat	cccgggagga	gatgaccaag	60
aaccagggtca	gcctgacctg	cctgggtcaaa	ggcttctatc	ccagcgacat	cgccgtggag	120
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgctccccgt	gctggactcc	180
gacggctcct	tcttcctcgc	cagcaagctc	accgtggaca	agagcagggtg	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
ctctccctgt	ccccgggtaa	atga				324

<210> 374

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 374

gggcagcccc	gagaaccaca	ggtgtacacc	ctgcccccat	cccgggagga	gatgaccaag	60
aaccagggtca	gcctgacctg	cctgggtcaaa	ggcttctatc	ccagcgacat	cgccgtggag	120
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgctccccgt	gctggactcc	180
gacggctcct	tcgccctcgc	cagcaagctc	accgtggaca	agagcagggtg	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
ctctccctgt	ccccgggtaa	atga				324

<210> 375

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 375

Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu
1				5					10					15	
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
			20					25					30		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
			35				40					45			
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
			50			55					60				
Tyr	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
65					70					75				80	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				85					90					95	



WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
100 105

<210> 376  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 376  
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
1 5 10 15  
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
20 25 30  
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
35 40 45  
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
50 55 60  
Ala Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
65 70 75 80  
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
85 90 95  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
100 105

<210> 377  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 377  
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
1 5 10 15  
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
20 25 30  
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
35 40 45  
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
50 55 60  
Phe Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
65 70 75 80  
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
85 90 95  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
100 105

<210> 378  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 378  
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
1 5 10 15  
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 20 25 30  
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
 35 40 45  
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
 50 55 60  
 Tyr Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
 65 70 75 80  
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
 85 90 95  
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 100 105

<210> 379  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 379  
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
 1 5 10 15  
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
 20 25 30  
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
 35 40 45  
 Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe  
 50 55 60  
 Ala Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
 65 70 75 80  
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
 85 90 95  
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 100 105

<210> 380  
 <211> 1515  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 380  
 aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgtttca 60  
 gtcataattg ccagaggaca aattgtttct tcccagttct cagcaatcct gtctgcatct 120  
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcaactg 180  
 taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctgggt 240  
 tctggagtcc ctgctcgctt cagtggcagt gggctctgga cctcttactc tctcacaatc 300  
 agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccac 360  
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420  
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480  
 aggcctgggg cctcagtga gattgtcctgc aaggcttctg gctacacatt taccagttac 540  
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
 gacaaatcct ccagcacagc ctacatgcag ctccagcagg tgacatctga agactctgct 720  
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgt 780  
 ggcacagggg ccacggtcac cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840  
 cacacatccc caccgtcccc agcacctgaa ctctctgggg gaccgtcagt ctctctcttc 900  
 ccccctgagc ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtgggt 960  
 gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020  
 gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggt 1080  
 agcgtctcca ccgtctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

```
tccaacaaag ccctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 1260
agcctgacct gcctgggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcgccctct atagcaagct caccgtggac aagagcagggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tccccgggta aatga 1515
```

<210> 381  
<211> 1521  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

```
<400> 381
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgtttca 60
gtcataattg ccagaggaca aattgtttct tcccagctctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgactggt 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcacaatc 300
agcagagtgg aggttgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgt 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatactt ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaactctc tgacaaaact 840
cacacatccc caccgtcccc agcacctgaa ctccctggggg gaccgtcagt cttcctcttc 900
cccccaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgctgtgtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgtgtc 1080
agcgtcctca cgtctctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 1260
agcctgacct gcctgggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttctacctct atagcaagct caccgtggac aagagcagggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tccccgggta aatgatctag a 1521
```

<210> 382  
<211> 1515  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

```
<400> 382
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgtttca 60
gtcataattg ccagaggaca aattgtttct tcccagctctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgactggt 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcacaatc 300
agcagagtgg aggttgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgt 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatactt ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgcg 720
```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

```
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaactctt tgacaaaact 840
cacacatccc caccgtcccc agcacctgaa ctccctgggg gaccgtcagt ctccctcttc 900
ccccaaaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgctgtggtg 960
gtggacgtga gccacgaaga ccttgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 1260
agcctgacct gcctgggtcaa aggtcttctat cccagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcttctctg ccagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgtctcg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tccccgggta aatga 1515
```

<210> 383  
<211> 1515  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide

```
<400> 383
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgtctca 60
gtcataattg ccagaggaca aattgttctc tcccagtcct cagcaatcct gtctgcatct 120
ccaggggaga aggtcacat gacttgcagg gccagctcaa gtgtaagtta catgactgtg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggctctgga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgtgggt 420
ggatctggag gagtggggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatactc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaactctt tgacaaaact 840
cacacatccc caccgtcccc agcacctgaa ctccctgggg gaccgtcagt ctccctcttc 900
ccccaaaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgctgtggtg 960
gtggacgtga gccacgaaga ccttgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 1260
agcctgacct gcctgggtcaa aggtcttctat cccagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttctacctcg ccagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgtctcg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tccccgggta aatga 1515
```

<210> 384  
<211> 1515  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide

```
<400> 384
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgtctca 60
gtcataattg ccagaggaca aattgttctc tcccagtcct cagcaatcct gtctgcatct 120
ccaggggaga aggtcacat gacttgcagg gccagctcaa gtgtaagtta catgactgtg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggctctgga cctcttactc tctcacaatc 300
```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtgagg ttttaaccca 360  
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgt 420  
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
 aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
 aatattgact gggtaaaagca gacacctaga cagggccttg aatggatttg agctatttat 600  
 ccaggaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actgactgta 660  
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgctg 720  
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
 ggcacagggg ccaagggtcac cgtctcttct gatcaggagc ccaaactctt tgacaaaact 840  
 cacacatccc caccgtcccc agcacctgaa ctctggggg gaccgtcagt cttcctcttc 900  
 cccccaaaac ccaaggacac cctcatgatc tcccggaacc ctgaggtcac atgctgtgtg 960  
 gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggtgtggag 1020  
 gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080  
 agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140  
 tccaacaaag cctctccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200  
 cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 1260  
 agcctgacct gcctgggtcaa aggccttctat cccagcgaca tcgccgtgga gtgggagagc 1320  
 aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380  
 ttcgccctcg ccagcaagct caccgtggac aagagcaggt ggacgaggg gaacgtcttc 1440  
 tcatgtctcg tgatgcatga ggctctgcac aaccactaca cgagaagag cctctccctg 1500  
 tccccgggta aatga 1515

<210> 385  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 385  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Tyr Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 386  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polypeptide

<400> 386  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Tyr Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 387  
 <211> 500  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> fusion polypeptide

<400> 387  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Ala Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 388  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 388  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95



WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
                   100                  105                  110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
                   115                  120                  125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
                   130                  135                  140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
                   145                  150                  155                  160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
                   165                  170                  175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
                   180                  185                  190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
                   195                  200                  205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
                   210                  215                  220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
                   225                  230                  235                  240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
                   245                  250                  255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
                   260                  265                  270  
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu  
                   275                  280                  285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
                   290                  295                  300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
                   305                  310                  315                  320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
                   325                  330                  335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
                   340                  345                  350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
                   355                  360                  365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
                   370                  375                  380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
                   385                  390                  395                  400  
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
                   405                  410                  415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
                   420                  425                  430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
                   435                  440                  445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Ala Ser Lys Leu Thr  
                   450                  455                  460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
                   465                  470                  475                  480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
                   485                  490                  495  
 Ser Pro Gly Lys  
                   500

<210> 389  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 389  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
   1                  5                  10                  15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
                   20                  25                  30

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Ala Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 390  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' oligo to mutat IgG1

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<400> 390  
gttggtgac aggagcccaa atcttctgac aaaactcaca catg 44

<210> 391  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' oligo to mutate IgG1

<400> 391  
gttggtgac aggagcccaa atcttctgac aaaactcaca catctccacc gtgc 54

<210> 392  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' oligo to mutate IgG1

<400> 392  
gttggtgac aggagcccaa atcttctgac aaaactcaca catgtccacc gtccccagca 60  
cct 63

<210> 393  
<211> 1521  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 393  
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgccttca 60  
gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct 120  
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
taccagcaga agccaggatc ctcccccaaa ccttggattt atgccccatc caacctggct 240  
tctggagtcg ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
agcagagtgg aggtgaaga tgctgccact tttactgccc agcagtgagg ttttaaccca 360  
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
aatatgcact gggtaaagca gacacctaga cagggccttg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgag 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840  
cacacatgcc caccgtgccc agcacctgaa ctcttggggg gaccgtcagt cttcctcttc 900  
ccccaaaac ccaaggacac cctcatgac tcccggacc ctgaggtcac atgctgggtg 960  
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcggtggag 1020  
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080  
agcgtcctca ccgtcctgca ccagactgg ctgaatggca agaggtacaa gtgcaaggtc 1140  
tccaacaaag ccctcccagc ccccatcgag aaaacaatct tcccgggatg agctgaccaa gaaccaggtc 1260  
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260  
agcctgacct gcctgggtcaa aggtcttctat cccagcgaca tcgcccgtga gtgggagagc 1320  
aatgggcagc cggagaacaa ctacaagacc acgctctccg tgctggactc cgacggcttc 1380  
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcagg gaacgtcttc 1440  
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
tctccgggta aatgatctag a

1521

<210> 394  
<211> 1521  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 394  
aagcttgccg ccattggattt tcaagtgcag attttcagct tcctgctaatt cagtgccttca 60  
gtcataaattg ccagaggaca aattgttctc tcccagtcctc cagcaatcct gtctgcatct 120  
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240  
tctggagtcc ctgctcgctt cagtggcagt gggctcggga cctcttactc tctcacaatc 300  
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtgagg ttttaaccca 360  
ccacggttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg 780  
ggcacagggg ccccggtcac cgtctcttct gatcaggagc ccaaactctg tgacaaaact 840  
cacacatctc caccgtgccc agcacctgaa ctctggggg gaccgtcagt cttcctcttc 900  
cccccaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtgggtg 960  
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcggtggag 1020  
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080  
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140  
tccaacaaag cctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200  
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260  
agcctgacct gcctgggtcaa aggttcttat cccagcagca tcgcccgtgga gtgggagagc 1320  
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380  
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440  
tcattgctcc tgatgcata ggtctgcac aaccactaca cgcagaagag cctctccctg 1500  
tctccgggta aatgatctag a

<210> 395  
<211> 1521  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 395  
aagcttgccg ccattggattt tcaagtgcag attttcagct tcctgctaatt cagtgccttca 60  
gtcataaattg ccagaggaca aattgttctc tcccagtcctc cagcaatcct gtctgcatct 120  
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240  
tctggagtcc ctgctcgctt cagtggcagt gggctcggga cctcttactc tctcacaatc 300  
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtgagg ttttaaccca 360  
ccacggttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg 780  
ggcacagggg ccacggtcac cgtctcttct gatcaggagc ccaaactctg tgacaaaact 840  
cacacatgac caccgtcccc agcacctgaa ctctggggg gaccgtcagt cttcctcttc 900  
cccccaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtgggtg 960  
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcggtggag 1020  
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140  
 tccaacaaag ccttccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200  
 cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260  
 agcctgacct gcctgggtcaa aggtcttctat cccagcgaca tcgccgtgga gtgggagagc 1320  
 aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacgggtcc 1380  
 ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440  
 tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500  
 tctccgggta aatgatctag a 1521

<210> 396  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 396  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Cys Pro Cys Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 385 390 395 400  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 397  
 <211> 500  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> fusion polypeptide

<400> 397  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Cys Asp Lys Thr His Thr Ser Pro Cys Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 Ser Pro Gly Lys  
 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500

<210> 398  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polypeptide

<400> 398  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 260 265 270  
 Cys Asp Lys Thr His Thr Cys Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 399  
 <211> 793  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polynucleotide

<400> 399  
 atgttgata catctcagct ccttgggctt ttactcttct ggatttcagc ctccagaagt 60  
 gacatagtgc tgactcagac tccagccact ctgtctctaa ttcctggaga aagagtcaca 120  
 atgacctgta agaccagtca gaatattggc acaatcttac actggtatca ccaaaaacca 180  
 aaggaggctc caagggtctc catcaagtat gcttcgcagt ccattcctgg gatcccctcc 240  
 agattcagtg gcagtggttc ggaaacagat ttcactctca gcatcaataa cctggagcct 300  
 gatgatatcg gaatttatta ctgtcaacaa agtagaagct ggcctgtcac gttcgggtcct 360  
 ggcaccaagc tggagataaa acgggggtggc ggtggctcgg gcggaggtgg gtcgggtggc 420  
 ggcggatctc aggtcaagct gcagcagctc ggttctgaac tagggaaacc tggggcctca 480  
 gtgaaactgt cctgcaagac ttcaggctac atattcacag atcactatat ttcttgggtg 540  
 aaacagaagc ctggagaaag cctgcagtgg ataggaaatg tttatgggtg aaatggtgg 600  
 acaagctaca atcaaaaatt ccagggcaag gccacactga ctgtagataa aatctctagc 660  
 acagcctaca tggaaactcag cagcctgaca tctgaggatt ctgccatcta ttactgtgca 720  
 agaaggccgg tagcgacggg ccatgctatg gactactggg gtcaggggat ccaagttacc 780  
 gtctcctctg atc  
 793

<210> 400  
 <211> 264  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polypeptide



WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<400> 400  
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe Trp Ile Ser  
1 5 10 15  
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser  
20 25 30  
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn  
35 40 45  
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro  
50 55 60  
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser  
65 70 75 80  
Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn  
85 90 95  
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg  
100 105 110  
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg  
115 120 125  
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln  
130 135 140  
Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser  
145 150 155 160  
Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr  
165 170 175  
Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly  
180 185 190  
Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln  
195 200 205  
Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met  
210 215 220  
Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala  
225 230 235 240  
Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly  
245 250 255  
Ile Gln Val Thr Val Ser Ser Asp  
260

<210> 401  
<211> 36  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> oligonucleotide primer

<400> 401  
gttggtgatc agccagttcc ctcaactcca cctacc

36

<210> 402  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide primer

<400> 402  
gttggtttcg aaggatccgc gtccacctcc gccatgacaa caga

44

<210> 403  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<223> oligonucleotide primer

<400> 403  
gttggttttcg aaggatccgc ttaccgga gacagggaga ggctctt 47

<210> 404  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide primer

<400> 404  
gttgtagat ctggagccca aatcttgta caaactcac acatg 45

<210> 405  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide primer

<400> 405  
gttggtgatc cttcgaacc gttcctggtg ctgctgcact cgggtgctg 48

<210> 406  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 406  
gttggtatcg atctcgagtt atcaggacgc ttcggaggta gatgcgtc 48

<210> 407  
<211> 657  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 407  
gtggatcctt cgaaccggtt cctggtgctg ctgcactcgg tgcgtccag cctgtcgagc 60  
agcgagctga ccgagctcaa gttcctatgc ctcgggcgcg tgggcaagcg caagctggag 120  
cgctgtcaga gcggcctaga cctcttctcc atgctgctgg agcagaacga cctggagccc 180  
gggcacaccg agctcctgcg cgagctgctc gcctccctgc ggcgccacga cctgctgcgg 240  
cgctgtcagc acttcgaggc gggggcgggc gccggggccg cgcctgggga agaagacctg 300  
tgtgcagcat ttaacgtcat atgtgataat gtggggaaag attggagaag gctggctcgt 360  
cagctcaaag tctcagacac caagatcgac agcatcgagg acagataccc ccgcaacctg 420  
acagagcggtg tgcgggagtc actgagaatc tggaagaaca cagagaagga gaacgcaaca 480  
gtggcccacc tgggtggggc tctcagggtc tgccagatga acctggtggc tgacctggta 540  
caagagggtc agcaggcccg tgacctccag aacaggagtg gggccatgtc cccgatgtca 600  
tggaactcag acgcatctac ctccgaagcg tcctgataac tcgagatcga taacaac 657

<210> 408

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 408

```

Val Asp Pro Ser Asn Pro Phe Leu Val Leu Leu His Ser Val Ser Ser
 1      5      10      15
Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly
 20      25      30
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
 35      40      45
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
 50      55      60
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
 65      70      75      80
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly
 85      90      95
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly
100      105      110
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys
115      120      125
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val
130      135      140
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr
145      150      155      160
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val
165      170      175
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
180      185      190
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser
195      200      205
Glu Ala Ser
210

```

<210> 409

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 409

gttggtgatc ctcccttttg ggtgctggtg gtggttggtg tcctggcttg ctatagcttg 60

<210> 410

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 410

gttggttcga acccagaaaa taataaaggc cactgttact agcaagctat agcaagccag 60

<210> 411

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

```

<400> 411
gttggtggatc ctcccttttg ggtgctggtg gt 32
<210> 412
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 412
gttggttcga acccagaaaa taataaaggc cac 33
<210> 413
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 413
gttggtggatc ctctgctcc catcctgg 28
<210> 414
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 414
gttggttcga acggcaaagc agtaggtcag gc 32
<210> 415
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 415
gttggtggatc cttcgaaccc attcctggtg ctgctgcact cgctg 45
<210> 416
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 416
gttggtatcg atctcgagtc agggtgttc tgaggaagac ac 42
<210> 417
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 417

```

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
gtggatcctt cgaacatgga cccattcctg gtgctgctgc actcgcgtgc cggcagcctg 60  
tcggggcaacg atctgatgga gctcaagttc ttgtgccgcg agcgcgtgag caaacgaaag 120  
ctggagcgcg tgcagagtgg cctggacctg ttcacgggtg tgctggagca gaacgacctg 180  
gagcgcgggc acaccgggct gctgcgcgag ttgttgccct cgctgcgccg acacgatcta 240  
ctgcagcgcc tggacgactt cgaggcgggg acggcgaccg ctgcgcccc gggggaggca 300  
gatctgcagg tggcatttga cattgtgtgt gacaatgtgg ggagagactg gaaaagactg 360  
gcccgcgagc tgaaggtgtc tgaggccaag atggatggga ttgaggagaa gtacccccga 420  
agtctgagtg agcgggtaag ggagagtctg aaagtctgga agaattgctga gaagaagaac 480  
gcctcgggtg ccggactggt caaggcgctg cggacctgca ggctgaatct ggtggctgac 540  
ctggtggaag aagcccagga atctgtgagc aagagtgaga atatgtcccc agtactaagg 600  
gattcaactg tgtcttcctc agaaacaccc tgactcgaga tcgat 645

<210> 418  
<211> 210  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 418  
Val Asp Pro Ser Asn Met Asp Pro Phe Leu Val Leu Leu His Ser Leu  
1 5 10 15  
Ser Gly Ser Leu Ser Gly Asn Asp Leu Met Glu Leu Lys Phe Leu Cys  
20 25 30  
Arg Glu Arg Val Ser Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu  
35 40 45  
Asp Leu Phe Thr Val Leu Leu Glu Gln Asn Asp Leu Glu Arg Gly His  
50 55 60  
Thr Gly Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu  
65 70 75 80  
Leu Gln Arg Leu Asp Asp Phe Glu Ala Gly Thr Ala Thr Ala Ala Pro  
85 90 95  
Pro Gly Glu Ala Asp Leu Gln Val Ala Phe Asp Ile Val Cys Asp Asn  
100 105 110  
Val Gly Arg Asp Trp Lys Arg Leu Ala Arg Glu Leu Lys Val Ser Glu  
115 120 125  
Ala Lys Met Asp Gly Ile Glu Lys Tyr Pro Arg Ser Leu Ser Glu  
130 135 140  
Arg Val Arg Glu Ser Leu Lys Val Trp Lys Asn Ala Glu Lys Lys Asn  
145 150 155 160  
Ala Ser Val Ala Gly Leu Val Lys Ala Leu Arg Thr Cys Arg Leu Asn  
165 170 175  
Leu Val Ala Asp Leu Val Glu Glu Ala Gln Glu Ser Val Ser Lys Ser  
180 185 190  
Glu Asn Met Ser Pro Val Leu Arg Asp Ser Thr Val Ser Ser Glu  
195 200 205  
Thr Pro  
210

<210> 419  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 419  
gttgtggatc cttcgaacat ggagaacaac aaaacctcag tggattca

48

<210> 420  
<211> 44  
<212> DNA  
<213> Artificial Sequence

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> oligonucleotide

<400> 420

gttgttatcg atctcgagct agtgataaaa gtacagttct ttcg

44

<210> 421

<211> 46

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 421

gttgtttcga acatggattt ccagagttgt ctttatgcta ttgctg

46

<210> 422

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 422

gttgttatcg atctcgagtc attagggagg gaagaagagc ttcttccg

48

<210> 423

<211> 45

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 423

gttggtgatc cttcgaacat ggagaacact gaaaactcag tggat

45

<210> 424

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 424

gttgttatcg atctcgagtt agtgataaaa atagagttct tttgtgag

48

<210> 425

<211> 45

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 425

gttggtgatc cttcgaacat ggacttcagc agaaatcttt atgat

45

<210> 426

<211> 48

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 426

gttggtatcg atgcatgctc aatcagaagg gaagacaagt ttttttct

48

18

EXPRESS MAIL NO:

1